AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1-25. (cancelled)

26. (previously presented) A method for analyzing or amplifying a nucleic acid sequence, comprising analyzing or amplifying a nucleic acid with an S3P primer.

27. (previously presented) The method according to claim 26, wherein said S3P primer is in combination with at least one AFLP primer.

28. (currently amended) The method according to claim 26, wherein the nucleic acid sequence comprises a restriction fragment to which one adapter sequence has been ligated.

29. (previously presented) The method according to claim 28, in which the restriction fragment to which the adapter sequence has been ligated is part of a mixture of adapter-ligated restriction fragments.

30. (previously presented) The method according to claim 26, in which the nucleic acid sequence contains or is suspected to contain, an intron-exon junction and/or a splice site.

31. (previously presented) The method according to claim 26, in which the restriction fragment is derived from

genomic DNA, mitochondrial DNA, chloroplast DNA, recombinant DNA or unprocessed heteronuclear mRNA.

32. (previously presented) The method according to claim 26, wherein the S3P primer is in an intron-to-exon orientation or in an exon-to-intron orientation.

33. (currently amended) The method according to claim [[26]] 27, wherein the AFLP primer contains at least one selective nucleotide at its 3' end.

34. (previously presented) The method according to claim 26, wherein the S3P primer comprises a conserved splice site border sequence or at least part of a consensus sequence.

35. (previously presented) The method according to claim 34, wherein the S3P primer further comprises a random sequence.

36. (previously presented) The method according to claim 26, wherein S3P primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns, and splice sites that are identified using computer based splice site identification methods.

37. (previously presented) The method according to claim 26, wherein the S3P primer contains a total of between 8 and 20 nucleotides.

38. (previously presented) The method according to claim 26, wherein between 4 and 10 nucleotides present in the S3P

primer are complementary to the conserved region or consensus sequence of the splice site.

39. (previously presented) The method according to claim 26, wherein the consensus sequence is $X_1X_2GTX_3X_4X_5X_6$, wherein X_1, X_2, X_3, X_4, X_5, X_6 are independently selected from the group consisting of A,C,T, or G.

40. (previously presented) The method according to claim 39, wherein the consensus sequence is AGGTAAGT.

41. (previously presented) A method for analyzing a nucleic acid sequence, comprising:

(a) amplifying an adapter-ligated restriction fragment generated from the nucleic acid to be analysed, using one or more S3P-primers and optionally an AFLP-primer to amplify the nucleic acid sequence; and optionally comprising the further step of:

(b) detecting the amplified nucleic acid sequences thus obtained.

42. (previously presented) A method for analyzing a nucleic acid sequence, the method comprising the steps of:

(a) restricting the starting nucleic acid with a restriction endonuclease to provide a mixture of restriction fragments;

(b) ligating the restriction fragments thus obtained to at least one adapter;

(c) amplifying the mixture of adapter-ligated restriction fragments thus obtained with one or more S3P-primers

and optionally at least one AFLP-primer to provide a mixture of amplified restriction fragments; and optionally comprising the further step of

(d) detecting the amplified restriction fragments thus obtained.

43. (previously presented) A method for the amplification of at least one restriction fragment obtained from a starting DNA, comprising:

(a) digesting the starting DNA with at least one restriction endonuclease, thereby providing one or more restriction fragments;

(b) ligating at least one oligonucleotide adapter to one or both ends of the restriction fragments to provide adapter-ligated restriction fragments;

(c) providing a primer set comprising one or more S3P primers and optionally at least one AFLP primer;

(d) contacting the adapter-ligated restriction fragments with the set of primers;

(e) amplifying the adapter-ligated restriction fragments with the set of primers; and

(f) recovery of any amplified DNA fragments.

44. (previously presented) A method for providing a PCR primer or a pair of PCR primers for use in the amplification of a PCR fragment spanning a splice site-associated genomic polymorphism, comprising:

a) identification of a fragment containing the splice site-associated genomic polymorphism, whereby the fragment is amplified by the combined use of one or more S3P primers and optionally at least one first AFLP primer for a first restriction enzyme used for AFLP template preparation;

b) sequencing the polymorphic fragment;

c) synthesizing a first PCR-primer corresponding to a sequence flanking the splice site sequence at the 3' end;

d) optionally, amplifying a fragment comprising the splice site-associated genomic polymorphism and sequences flanking the splice site-associated genomic polymorphism at its 5'-end, using the first PCR-primer and a second AFLP primer for a second restriction enzyme used for AFLP template preparation; and,

e) optionally, synthesizing a second PCR-primer corresponding to a sequence flanking the splice site sequence at the 5'end.

45. (previously presented) A method for providing a PCR-primer, comprising:

a) restricting a nucleic acid sequence with at least one restriction endonuclease to provide a mixture of restriction fragments;

b) ligating the restriction fragments thus obtained to at least one adapter;

c) amplifying the mixture of adapter ligated restriction fragments thus obtained with at least one S3P primer and optionally at least one first AFLP-primer to provide a mixture of amplified restriction fragments;

d) detecting at least one of the amplified restriction fragments thus obtained;

e) identifying at least one splice site-associated polymorphic fragment;

f) determining the sequence of said polymorphic fragment;

g) synthesizing a first PCR-primer corresponding to a sequence flanking the splice site sequence at the 3' end;

h) optionally, amplifying a fragment comprising the splice site and at least part of the 5'-flanking sequence using the first PCR-primer and a second AFLP primer used in AFLP template preparation; and

i) optionally, synthesizing a first PCR-primer corresponding to a sequence flanking the splice site sequence at the 5'end.

46. (previously presented) A kit comprising at least one S3P primer and optionally at least one AFLP primer.

47. (currently amended) A kit comprising PCR-primers obtained by a method according to claim [[40]] 44.

48. (previously presented) A method for the enrichment of a sample for nuclear or organelle derived amplification

products, comprising enriching the sample according to a method according to claim 43.

49. (new) The method according to claim 41, wherein the S3P-primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns, and splice sites that are identified using computer based splice site identification methods.

50. (new) The method according to claim 42, wherein the S3P-primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns, and splice sites that are identified using computer based splice site identification methods.

51. (new) The method according to claim 43, wherein the S3P-primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns, and splice sites that are identified using computer based splice site identification methods.

52. (new) The method according to claim 44, wherein the S3P-primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns,

and splice sites that are identified using computer based splice site identification methods.

53. (new) The method according to claim 45, wherein the S3P-primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns, and splice sites that are identified using computer based splice site identification methods.

54. (new) A kit comprising PCR-primers obtained by the method according to claim 45.